

**DRAFT****Summary of the Claims:**

1. Previously Cancelled
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29. Previously Cancelled

30. (Currently Amended) A computer readable memory that upon execution by a computer processor carries out the following functions:  
a) alters at least one supersecondary structure parameter value of a protein backbone structure from a protein said protein backbone structure having at least one non-variable residue and a plurality of variable residue positions;

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- b) correlates a group of potential rotamers for residue positions of said protein backbone structure[;]  
for a plurality of said variable residue positions of said protein; and
- c) analyzes the interactions of each potential rotamers from said group with each other potential rotamer from said group with all or part of the remainder of said protein backbone structure and a rotamer at said at least one non-variable residue position to generate a set of optimized protein sequences.

- 31. Cancelled
- 32. Cancelled
- 33. Cancelled
- 34. Cancelled
- 35. Cancelled

36. (Currently Amended) A computer readable memory that upon execution by a computer processor carries out the following functions:

- a) alters at least one supersecondary structure parameter value of a protein backbone structure from a protein;
- b) correlates a group of potential amino acids side chains for residue positions of said protein backbone structure; and
- c) analyzes the interactions of each potential amino acids side chains from said group with each other potential amino acid side chain from said group with all or part of the remainder of said protein backbone structure and a rotamer at said at least one non-variable residue position to generate a set of optimized protein sequences.

- 37. Cancelled
- 38. Cancelled
- 39. Cancelled

40. (Currently Amended) A computer readable memory that upon execution by a computer processor carries out the following functions:

- (Aa) [receiving] receives a protein backbone structure with variable residue positions from a protein;
- (Bb) [altering] alters at least one supersecondary structure parameter value of said protein backbone structure prior to establishing a group of potential amino acids;
- (Cc) [establishing] establishes a group of potential amino acids for each of said variable residue positions, wherein a first group for a first variable position has a first set of at least two amino acid side chains, and wherein a second group for a second variable position has a second set of at least two different amino acid side chains; and wherein said sets are different; and

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(Dd) [analyzing] analyzes the interactions of [all or part of]each [of said amino acids with all or part of the remainder of said protein backbone structure] potential amino acid side chains from said group with each other potential amino acid side chain from said group with all or part of the remainder of said protein backbone structure and a rotamer at said at least one non-variable residue position to generate a set of optimized protein sequences.

41. (Previously Added) A computer readable memory according to claim 40 wherein said first and second sets of amino acids are different.

42. (Previously Added) A computer readable memory according to claim 40 wherein said first and second sets of amino acids are the same.

43. (Currently Amended) A computer readable memory that upon execution by a computer processor carries out the following functions:

- a) [receiving] receives a protein backbone structure with variable residue positions;
- b) [altering] alters at least one supersecondary structure parameter value of said protein backbone structure prior to establishing a group of potential [rotamers] residue positions;
- c) [establishing] establishes a group of potential rotamers for each of said variable residue positions, wherein the group for at least one variable residue position has rotamers of at least two different amino acid side chains, and wherein at least one of said amino acid side chains is from a hydrophilic amino acid; and,
- d) [analyzing the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences, wherein said analyzing step includes the use of at least one scoring function] analyzes the interaction of potential rotamers from said group with each other potential rotamers from said group with all or part of the remainder of said protein backbone structure and a rotamer at said at least one non-variable residue position to generate a set of optimized protein sequences, wherein said analyzing step includes the use of at least one scoring function.

44. (Currently Amended) A computer readable memory according to claim 43 wherein said [first and second sets of rotamers] amino acid side chains are different.

45. (Currently Amended) A computer readable memory according to claim 43 wherein said [first and second sets of rotamer] amino acid side chains are the same.

46. (Previously Added) A computer readable memory according to claim 43 wherein said hydrophilic amino acid is selected from the group consisting of serine, threonine, aspartic acid, asparagine, glutamine, glutamic acid, arginine, lysine, and histidine.

47. (Previously Added) A computer readable memory according to claims 40 or 43 wherein step d) further

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comprises a ranking module.

48. Cancelled

49. (New) A computer readable memory according to claim 30 wherein step c) further comprises a ranking module.

50. (New) A computer readable memory according to claim 49 wherein said ranking module includes a van der Waals scoring function component.

51. (New) A computer readable memory according to claim 49 wherein said ranking module includes an atomic solvation scoring function component.

52. (New) A computer readable memory according to claim 49 wherein said ranking module includes a hydrogen bond scoring function component.

53. (New) A computer readable memory according to claim 49 wherein said ranking module includes a secondary structure scoring function component.

54. (New) A computer readable memory according to claim 30 that further assess the correspondence between potential energy test results and theoretical potential energy data.

55. (New) A computer readable memory according to claims 30, 36 or 49-53 further comprising physically generating at least one member of said set of optimized protein sequences and experimentally testing said sequence for a desired function.